Please replace the paragraph beginning on page 37, line 17 with the following rewritten paragraph:

--PPA = Paired Probe Array

Oligo targets: a, b, c and d are placeholders for different sequences. Actual sequences are given in Fig. 4A.

Buffer A= 6xSSPE, 0.005% Triton X-100

Buffer B= 2.4M Tetraethylammonium Bromide, 10mM Tris pH 7.8, 1mM EDTA, 0.05% Triton X-100

Buffer C= 2.4M Methyltriethylammonium Bromide, 10mM Tris pH 7.8, 1mM EDTA, 0.05% Triton X-100

Label: F = fluorescein, P = phycoerythrin-streptavidin--

IN THE CLAIMS:

Please cancel claims 1-9 and 11 without prejudice or disclaimer. Please add the following new claims as indicated:

19. (New) An array, comprising:

(a) a support comprising a first and a second discrete region;

(b) a pool of probes bound to the first discrete region comprising a first and a second component probe respectively complementary to nonoverlapping segments of a mRNA molecule; and

(c) a mismatch probe or pool of mismatch probes bound to the second discrete region, wherein

the mismatch probe has the same sequence as one of the first and second component probes except for a single base mismatch; and

the pool of mismatch probes comprises a first and a second mismatch probe that respectively have the same sequence as the first and second component probe except for a single base mismatch.

20. (New) The array of claim 19, wherein

the first and second discrete region are one of a plurality of first and second discrete regions;

the pool of probes is one of a plurality of different pools of probes, the first and second component probes in different pools complementary to nonoverlapping segments from different mRNA molecules, with different pools bound to different first discrete regions; and

the array comprises a mismatch probe or pool of mismatch probes corresponding to each of the different pools of probes, mismatch probes or mismatch pool of probes corresponding to different pools bound at different second discrete regions.

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21. (New) An array, comprising a plurality of sets of nucleic acid probes, each set comprising a plurality of probe pools bound to a different region of a support, each pool comprising

a first probe that is common to the probe pools within the set and complementary to a known marker located in a target nucleic acid; and

a second probe that differs in sequence from the first probe; and

wherein the first probes differ in sequence between the different sets.

22. (New) The array of claim 21, wherein the first probes in different sets are complementary to different markers on the target nucleic acid.

23. (New) The array of claim 21, wherein for any particular set of probes the second probes are the same length and collectively represent all possible sequences having that length.

24. (New) An array comprising a plurality of different nucleic acid probe mixtures bound to different regions of a support, each mixture comprising an interrogation probe and a partner probe, wherein

the interrogation probes are complementary to a first segment of a reference nucleic acid that contains an interrogation position and identical to one another except at the interrogation position, with different interrogation probes having a different one of the four nucleotide bases at the interrogation position;

the partner probe is complementary to a second segment of the reference nucleic acid that does not overlap the first segment; and

different probe mixtures have different interrogation probes.

25. (New) The array of claim 24, wherein different probe mixtures contain the same partner probe.

26. (New) The array of claim 24, wherein different probe mixtures contain different partner probes that bind to different second segments.

27. (New) The array of claim 24, wherein the first and second segments are separated from one another on the reference sequence.

28. (New) The array of claim 24, wherein the first and second segments are immediately adjacent one another on the reference sequence.

29. (New) A method of analyzing gene expression, comprising:

(a) providing an array comprising

(i) a plurality of different pools of probes each comprising a first and a second component probe respectively complementary to nonoverlapping segments of a known mRNA molecule, different pools of probes complementary to different known mRNA molecules and bound to different discrete regions of a support; and

(ii) a mismatch probe or pool of mismatch probes corresponding to each of the plurality of different probe pools, wherein

the mismatch probe has the same sequence as one of the first and second component probes in the corresponding pool except for a single base mismatch; and

the pool of mismatch probes comprises a first and a second mismatch probe that respectively have the same sequence as the first and second component probe in the corresponding pool except for a single base mismatch; and

the mismatch probe or pool of mismatch probes that correspond to different pools are bound to different regions of the support and at regions distinct from the corresponding probe pools;

(b) hybridizing a sample comprising a population of mRNA or nucleic acids copied therefrom to the array; and

(c) comparing binding of members of the population to at least one of the pool of probes and the corresponding mismatch probe or pool of mismatched probes to determine at least one mRNA that is present in the sample.

30. (New) A method for analyzing a target nucleic acid sequence, comprising

(a) providing an array comprising a plurality of different nucleic acid probe mixtures bound to different regions of a support, each mixture comprising an interrogation probe and a partner probe, wherein

the interrogation probes are complementary to a first segment of a reference nucleic acid that contains an interrogation position and identical to one another except at the interrogation position, with different interrogation probes having a different one of the four nucleotide bases at the interrogation position;

the partner probe is complementary to a second segment of the reference nucleic acid that does not overlap the first segment; and

different probe mixtures have different interrogation probes;

(b) applying a sample comprising the target nucleic acid to the array; and

(c) determining the identity of the nucleotide base at the interrogation position of the target nucleic acid from the relative binding of the target nucleic acid to the different probe mixtures.